

FIGURE 1

GGCTGAGGGGAGGCCCGGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGA
GAGAAGCGCCTGCAGCCAACCAGGGTTCAGGCTGTGCTCACAGTTTCCTCTGGCGGCATGTAA
AGGCTCCACAAAGGAGTTGGGAGTTCAAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCC
CAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGA
AGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCCTCTGCCGGAGCCCT
CTGTGGAGGCAGAGCCAGTGGAGCCCCAGTGAAGGAGGCTGCTTGGCAGCCACCGGCCTGCA
ACTCAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATG
TGAGGAGCCGCCCCGGAGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGA
ATAACCACCATTTTGCAGGACC**ATG**AGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTG
CTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTTTGAGGGCACTGAGGAGGGCTC
GCCAAGAGAGTTTACCTTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGACAAGTGCA
CCTACACCTTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAG
CCTGAGGTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCT
GCTCAAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTG
TGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGCGGGTCACGCAGCTC
TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCAGCT
GGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAGGACC
TGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCCACAACCAATCAGAGATCATCGCGCAG
CTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCAGCCACCCCCCGCTGC
CCCCCCCCGGGTCTACCAACCACCCACCTACAACCGCATCATCAACCAGATCTCTACCAACG
AGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCTCTGCCCACTATGCCCACTCTC
ACCAGCCTCCCATCTTCCACCGACAAGCCGTGCGGGCCATGGAGAGACTGCCTGCAGGCCCT
GGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTCA
TGCAGGTGTGGTGGCAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTG
GATGGCTCTGTAACTTCTTCAGGAAGTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGA
CGGCGAATACTGGCTGGGCCTGGAGAACATTTACTGGCTGACGAACCAAGGCAACTACAAAC
TCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTCTTTGCAGAATACGCCAGTTTCCGC
CTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGCAATGCGGGTGA
CTCCTTTACATGGCACAACGGCAAGCAGTTCACCACCCCTGGACAGAGATCATGATGTCTACA
CAGGAACTGTGCCCCTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAAC
CTCAACGGGGTCTGGTACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTG
GGCTGAGTTCCGAGGAGGCTCTTACTCACTCAAGAAAGTGGTGATGATGATCCGACCGAACC
CCAACACCTTCCAC**TAAG**CCAGCTCCCCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCA
CCCTGGTCACGCTGGCCACAGCACAAAGAACAACCTCCTACCAGTTCATCCTGAGGCTGGGA
GGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAACCTGAATCGAT
ACGGTGTTTTCTGTCCCTCCTACTTTTCCTTCACACCAGACAGCCCTCATGTCTCCAGGACA
GGACAGGACTACAGACAACCTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA

2/75

FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA22779
><subunit 1 of 1, 493 aa, 1 stop
><MW: 57104, pI: 7.67, NX(S/T): 2
MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQ
QRVTGAICVNSKEPEVLLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLR
KESRNMNSRVLTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLEHKYQHL
ATLAHNQSEIIAQLEEHQCRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNL
KVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQR
HDPGGWTVIQRRLDGSVNFFRNWETYKQGGFNIDGEYWLGLENIYWLTNQGNKLLVTMEDW
SGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAYHQ
KGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSCLKKVVMMIRPNPNTFH

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Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 124-128

Tyrosine kinase phosphorylation sites.

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites.

amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347,
465-471, 473-479

Amidation site.

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature.

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins.

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins.

amino acids 275-292

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCGCCGCGCCGCCCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCCTAGAAGAGGGT
GTTCCCTCTTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT
GCGGCTAACAGGGCCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAATTCC
TCAACTCCAGGTTATGAAAACAGTACTTGGAAGTGAAGTACCTAAATGATCGTCTTTG
GTTGGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
GAAAAGTGTTCTGCCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

4/75

FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26846

<subunit 1 of 1, 117 aa, 1 stop

<MW: 12692, pI: 7.50, NX(S/T): 0

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ

AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK

Important features:

Signal peptide:

amino acids 1-16

N-myristoylation sites.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAA
GCCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCC**ATG**GCGGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTCACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
G**TAG**CCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGG
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

6/75

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCDKNKLNVSFVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGYLETSELTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

7/75

FIGURE 7

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACAT**TAG**

8/75

FIGURE 8

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
><subunit 1 of 1, 247 aa, 1 stop
><MW: 27702, pI: 10.36, NX(S/T): 2
MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLR
RQDPQLKGI VTRLYCRQGYLQMHPDGALDGTKDDSTNSTLFNLI PVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT
    
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N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 9

CTCGCAGCCGAGCGCGGCCGGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCA
GACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCT
GTGTCCAGACTGAGGCCCCATTTGCATTGTTTAACTACTTAGAAAATGAAGTGTTCAATTTT
TAACATTCTCCTCCAATTGGTTTAAATGCTGAATTACTGAAGAGGGGCTAAGCAAAACCAGGT
GCTTGCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGCGCTCTCCCGTGTCTCTCCA
CGACTCGCTCGGCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCCAGAGGAGGCCGA
CGTGCCCGAGCTCCTCCGGGGGTCCCGCCCGGAGCTTTCTTCTCGCCTTCGCATCTCCTCC
TCGCGCGTCTTGGAC**ATG**CCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTG
TCTTCCAAGCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGT
CAGGACAGTGTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATG
ATGTGTGTTAACC AAAATGGCGGGTATTTATGCATTCCCCGACAAACCCTGTGTATCGAGG
GCCCTACTCGAACCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCAC
TCTCAGCTCCAACTATCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATG
GATGAAAGCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCC
CACCCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGC
TTCTGGAAGGCCAGTGCTTAGACATTGATGAATGTGCTATGGTTACTGCCAGCAGCTCTGT
GCGAATGTTCTTGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGG
AAGGTCTTGCCAAGATGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAACCTGCGTCA
ACACCTACGGCTCTCTCATCTGCCGCTGTGACCCAGGATATGAACCTTGAGGAAGATGGCGTT
CATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAA
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GCTGCCAAGACATCAACGAATGTGAGCACAGGAACACACGTGCAACCTGCAGCAGACGTGC
TACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAG
GATCAGTGATAACCGCTGTATGTGTCTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTA
CCATCTTGTACCGGGACATGGACGTGGTGTGTCAGGACGCTCCGTTCCCGCTGACATCTTCCAA
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CCATCAAAGGGCCCCGGGAAATCCAGCTGGACTTGGAAATGATCACTGTCAACACTGTCATC
AACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTGCGCAGTACCCATTCT**TGAGC**
CTCGGGCTGGAGCCTCCGACGCTGCCTCTCATTGGCACCAAGGGACAGGAGAAGAGAGGAAA
TAACAGAGAGAATGAGAGCGACACAGACGTTAGGCATTTCTGCTGAACGTTTCCCCGAAGA
GTCAGCCCCGACTTCCTGACTCTCACCTGTACTATTGCAGACCTGTCAACCTGCAGGACTTG
CCACCCCCAGTTCCTATGACACAGTTATCAAAAAGTATTATCATTGCTCCCCTGATAGAAGA
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TTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCAAAGACCCGGGAGCTGGCGGGGAACCTT
GGGAGTAGCTAGTTTGTCTTTTTCGTACACAGAGAAGGCTATGTAAACAAACCACAGCAGGA
TCGAAGGGTTTTTAGAGAATGTGTTTCAAACCATGCCTGGTATTTTCAACCATAAAGAAG
TTTCAGTTGTCTTAAATTTGTATAACGGTTTAAATCTGTCTTGTTCACTTTTGTCTTTT
AAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGACACATGCTATGTTCTGTCTTCCC
AAACCCAGTCTCCTCTCCATTTTAGCCCAGTGTTTTCTTTGAGGACCCCTTAATCTTGCTTT
CTTTAGAATTTTACC CAATTGGATTGGAATGCAGAGGTCTCCAACTGATTAAATATTTGA
AGAGA

10/75

FIGURE 10

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQ
 NGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQ
 CVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPG
 SYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGS LICRCDPGYELEEDGVHCSDM
 DECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQG
 GFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMATT
 RYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGS
 SVIRLRIYVSQYPF

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,
 267-273, 310-316

Aspartic acid and asparagine hydroxylation sites.

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

11/75

FIGURE 11

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGAACACAGGTCCTTGTTGCTGCAGAGAAGCAGTTGTTTTGCTG
GAAGGAGGGAGTGCGCGGGCTGCCCCGGGCTCCTCCCTGCCGCCTCCTCTCAGTGGATGGTT
CCAGGCACCCTGTCTGGGGCAGGGAGGGCACAGGCCTGCACATCGAAGGTGGGGTGGGACCA
GGCTGCCCCCTCGCCCCAGCATCCAAGTCCTCCCTTGGGCGCCCCGTGGCCCTGCAGACTCTCA
GGGCTAAGGTCTCTGTTGCTTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGT
AGCTTGAAGGAGGCACCA**ATG**CAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCCTG
GCTCAGGCCTGCCCTGAGCCCTGCGACTGTGGGGAAAAGTATGGCTTCCAGATCGCCGACTG
TGCTACCGCGACCTAGAATCCGTGCCGCCTGGCTTCCCGGCCAATGTGACTACACTGAGCC
TGTCAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCTTCAGGGAGGTGCCCTGCTGCAG
TCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGGAGCCCTGGCCTCTCTGAG
CCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGCCTGGAGCGACCTGC
ACAACCTCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGC
GACGCCTTCCGCAGCCTCCGTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGACACAC
ATTGGCCGAGGGCACCTTCACCCCGCTCACCGCGCTGTCCCACCTGCAGATCAACGAGAACC
CCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCCTGACCACGGCCGTGTCC
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CCGCCTGCCGCCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGG
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GCCCCCTCAGCTTCACTGGCACATCCAGATACCCAGTGGCATTGTGGAGATCACCAGCCCCAA
CGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCCCTGTGGCCAGCTCCAGCCGCGCTTCC
AGGCCTTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGGAGGAAGGCACCTAC
AGCTGCCTGGCCACCAATGAGCTGGGCAGTGTGAGAGCTCAGTGGACGTGGCACTGGCCAC
GCCCCGTGAGGGTGGTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAA
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ATCTACCTCAGCCGTGCTGGGAACCCTGAGGCTGCAGTCGCAGAAGGGGTCCCTGGGCAGCT
GCCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCCTTCTTCTCCTCACCTCCTTCT**T**
AGCCCCACCCAGGGCTTCCCTAACTCCTCCCTTGCCCCCTACCAATGCCCTTTAAGTGCTG
CAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTACCTCT
CCTTCTAATCTCTTCTAGAGCACCTGCTATCCCCAACTTCTAGACCTGCTCCAAACTAGTGA
CTAGGATAGAATTTGATCCCCTAACCTCACTGTCTGCGGTGCTCATTGCTGCTAACAGCATTG
CCTGTGCTCTCCTCTCAGGGGCAGCATGCTAACGGGGCGACGTCCTAATCCAACCTGGGAGAA
GCCTCAGTGGTGGAATTCCAGGCACTGTGACTGTCAAGCTGGCAAGGGCCAGGATTGGGGGA
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GAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCCTGCT
CCTTGCTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAAA
TGTGGGGATCCAGGATGGCCTTCCTTCCTCTTACCCTTCCTCCCTCAGCCTGCAACCTCTAT
CCTGGAACCTGTCCTCCCTTTCTCCCCAACTATGCATCTGTTGTCTGCTCCTCTGCAAAGGC
CAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTTCTGATGCCAAAAAAAAAAAAAAAAA
AAGGGCGGCCGCGACTCTAGAGTCGACCT

FIGURE 12

MQELHLLWWALLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGFPANVTTLSSLNRL
PGLPEGAFREVPLLQSLWLAHNEIRTVAAGALASLSHLKSLDLSHNLISDFAWSDLHNLSAL
QLLKMSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCCTC
GIVWLKTWALTAVSIPEQDNIACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELR
PGFVLALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANG
SLIPDFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTV
DNEVQPSGPEDNVVIIYLSRAGNPEAAVAEGVPGQLPPGLLLLQSLLLFFFLTSF

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domain:

amino acids 403-418

N-glycosylation sites.

amino acids 51-55, 120-124, 309-313

Tyrosine kinase phosphorylation site.

amino acids 319-326

N-myristoylation sites.

amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329,
334-340, 350-356, 394-400

Amidation site.

amino acids 355-359

Leucine rich repeats.

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

Leucine rich repeat C-terminal domain.

amino acids 180-230

CCAGGCCGGGAGGCGGACGCGCCAGCCGCTCTAAACGGGAACAGCCCTGGCTGAGGGAGAGCTGC
AGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGC
AGCGAGGAGGTCTTGAGCAGCATGGCCCGGAGGAGCGCCTTCCCTGCCGCCGCGCTCTGGCT
CTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGCCGGGCCGCCGAGGAGGAGA
GCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGAAGAAGATATC
CTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTCAGAAAAGCGCAACAGAG
AATGCCAGCTATTCCCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGG
CAGAATACTTCTATGAATTCCCTGTCCCTGCGCTCCCTGGATAAAGGCATCATGGCAGATCCA
ACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCATCAGTTGTTCAAGTTGGTTT
CCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTTGAAGTGGATGTGATTGTTATGAATT
CTGAAGGCAACACCATTTCTCCAAACACCTCAAAATGCTATCTTCTTTAAACATGTCAACAA
GCTGAGTGCCCAGGCGGGTGCCGAAATGGAGGC'TTTTGTAATGAAAGACGCATCTGCGAGTG
TCCTGATGGGTTCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATG
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GACAAAGCAAAGTCTCAACCACCTGCTTTAATGGAGGGACCTGTTTCTACCCTGGAAAATG
TATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAAATGCCACAACCCTGTC
GAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCCAAAGTTACCAGGGAGAC
CTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAA
CAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCC
TCATACATGCCCTGAGGCCAGCAGGCGCCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAG
GCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGGTGA'ACTCCGACATCTGAAAC
GTTTTAAGTTACACCAAGTTCATAGCCCTTTGTTAACCTTTCATGTGTTGAATGTTCAAATAA
TGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGCT
GATATTTACTCTTCCCTTTTAAGTTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCT
TGTTTCAGTGCTTTTGGGACAGATTTTATATTATGTCAATTGATCAGGTAAATTTTTCAGTG
TGTAGTTGGCAGATATTTTCAAATTAACAATGCATTTATGGTGTCTGGGGGCAGGGGAACAT
CAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAATTTGGATGGTGCAGTTAATGT
TGAAGTTACAGCATTTTCAGATTTTATTGTCAGATATTTAGATGTTTGTTACATTTTAAAAA
TTGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATT
CAGTATTAAAAAATAAATAATTACACTGTGGTAGTGGCATTTAAACAATATAATATATTCTA
AACACAATGAAATAGGGAATATAATGTATGAACTTTTTGCATTGGCTTGAAGCAATATAATA
TATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTATACTGTTTGTATGTATAAAAT
AAAGGTGCTGCTTTTAGTTTTTTTGGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA

FIGURE 14

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMIPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNLILQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYFPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKSKGYQGDLCSKPV
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEEERRDP
PESNYIW

Signal sequence.

amino acids 1-28

N-glycosylation sites.

amino acids 88-92, 245-249

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

16/75

FIGURE 16

MMGLSLASAVLLASLLSLHLGTATRGSDISKTC CFQYSHKPLPWTWVRSYEFTSNSCSQRAV
IFTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features of the protein:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

CCGAGAACCTTTTGCACGCGCACAAACTACGGGGACGATTCTGATTGATTTTTTGGCGCTTTCGATCCACCCTCC
TCCCTTCTC**ATGG**GAAGCTTTGGGGACAAAGCGTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGC
CAGGACAGCGTCGGGAACAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTTCGTCGCTTTCATCGTCGCGC
TTCTGCTGCGGGTCCGGGTGTGACTCTGCCACCATCCCCCGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTG
CAGCAACAGAGGCGCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTG
TAACCCGTGCACAGAGGGGTGTGGATTACACCATTTGCTTCCAACAATTTGCCTTCTTGCCTGCTATGTACAGTTT
GTAAATCAGGTCAAACAAATAAAAGTTCCCTGTACCACGACCAGAGACACCGTGTGTAGTGTGAAAAAGGAAGC
TTCCAGGATAAAAACTCCCCTGAGATGTGCCGGACGCTGTAGAACAAGGTTGCCAGAGGAGTGGTCAAGGTCAG
TAATTGTACGCCCGGAGTGACATCAAGTGCAAAATGAATCAGCTGCCAGTTCCTCAGTGGGAAAAACCCAGCAG
CGGAGGAGACAGTGACCACCATCCTGGGGATGCTTGCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTTA
GTCATCATTTTTAGCTGTGGTTGTGGTTGGCTTTTTCATGTGCGGAAGAAATTCATTTCTTACCTCAAAGGCATCTG
CTCAGGTGGTGGAGGAGGTCCCGAACGTGTGCACAGAGTCCTTTTCCGGCGGCGTTCATGTCTTACAGAGTTC
CTGGGGCGGAGGACAATGCCCGCAACGAGACCTTGAGTAACAGATACTTGCAGCCACCCAGGTCCTCTGAGCAG
GAAATCCAAGGTCAAGAGCTGGCAGCTTAACAGGTGTGACTGTAGAGTGCAGGAGGAGGACAGCGCTGTGCT
GGAACAGGCAGAAGCTGAAGGGTGTCAAGGAGGAGGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACA
TCAGCACCTTGGCTGGATGCCTCGGCAACACTGGAAGAAGGACATGCAAAGGAAACAATTCAGGACCAACTGGTG
GGCTCCGAAAAGCTCTTTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCTTGCCTG**TGA**AAGAATCTCTTCAG
GAAACCAAGAGCTTCCCTCATTTACCTTTTTCTCTCAAAAGGGAAGCAGCCTGGAAGAAACAGTCCAGTCACTTG
CCCATGCCCCAACCAACTCTACTATCCAAATAGGGGCAGTTACCAATGGTCTAGAAACTTTGTTAAACGCATTG
GGAGTAATTTTTTATGAAATACTGCGTGTGATAAGCAAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGT
TATACGATTGTGTATTAAGGGTCGTTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCAGCACTTTGATAG
GCTGAGGCAGGTTGGATTGCTTGAAGTCTGGGAGTTTGAGACCAGCCTCATCAACACAGTGAAATCTCCATCTCAAT
TTAAAGAAGAAAAAGTGGTTTATAGGATGTCTTCTTTGCACTTCTTATCATATGACAGCAAGTCTTTTTTCTGC
TTCTTATATTGGCAAGCTCCATCTCTACTGGTGCTGCAATTAATGACATCTAACTACAGATGCCGCACAGCCAC
AATGCTTTTGCTTATAGTTTTTTAACTTTAGAACGGGATTATCTTGTATTACCTGTATTTTTCAGTTTTCGGATA
TTTTTGAAGTTAATGATGAGATTATCAAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTTACGAGGGTTT
GACTTAGAGTTTTTGAAGTTTAAAGTATAGGATTATGGGGCTTACCCCCAGCTTAATTAGAGAAACATTTATATG
CTTACTACTGTAGGCTGTACATCTCTTTCCGATTTTGTATAATGATGTAAACATGAAAAACCTTTAGAAAT
GCACCTTATTAGGCTGTTTACATGGTTGGCTGGATACAATCAGCAGTCAAAAATGACTAAAAATATAACTAGT
GACGGAGGGAGAAATCCTCCCTCTGTGGGAGGCACCTTACTGCATTCCAGTTCTCCCTCCTGCGCCCTGAGACTG
GACCAGGGTTTTGATGGCTGGCAGCTTCTCAAGGGGCAGCTTGTCTTACTTGTAAATTTTAGAGGTATATAGCCA
TATTTTATTTATAAATAAATATTTATTTATTTTATTTATAAGTAGATGTTTACATATGCCAGGATTTTGAAGAGC
CTGGTATCTTTGGGAAGCCATGTGTTCTGGTTGCTGTGGGACAGTCAAGTGGGACTGCATTTCCGACTTGTGTC
CACAGCATAGTGGACAGTGAGATTTAAGTTAGATCCGAGACTGCGAAGAGCTTCTCTTTCAAGCGCCATTACA
GTTGAACGTTAGTGAATCTTGAGCCTCATTTGGGCTCAGGGCAGAGCAGGTGTTTATCTGCCCCGGCATCTGCC
ATGGCATCAAGAGGGGAAGAGTGGACGGTGC'TTGGGAATGGTGTGAATGGTTGCCGACTCAGGCGATGGATGGGC
CCCTCTCGCTTCTGGTGGTCTGTGAAGTGAAGTCCCTGGGATGCCTTTAGGGCAGAGATTCCTGAGCTGCGTTT
TAGGGTACAGATTCCCTGGTTTGAGGAGCTTGGCCCCCTCTGAAGCATCTGACTCATCTCAGAGATATCAATCT
TAAACACTGTGACAACGGGATCTAAAATGGCTGACACATTTGTCTTGTGTACGTTCCATTATTTTTATTTAA
AACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACTCTTCTCCACAGTAGCCAGTCTGTTGGTAGGATAAATTA
CGGATATAGTCATTTCAAGGGTTTCAGTCTTTTCCATCTCAAGGCATTTGTGTGTTTTGTTCCGGGACAGTGGTTT
GCTGGGACAACAAGTTAGAAGTGCCTGAAGTTCGCACATTCAGATTGTTGTGCCATGGAGTTTTAGGAGGGGATG
GCCTTTCCGGTCTTTCGCACTTCCATCCTCTCCCACTTCCATCTGGCGTCCCACACCTTGTCCCCGCACTTCTG
GATGACACAGGGTGTGCTGCCCTCCTAGTCTTTGGCTTTGCTGGGCCTTCTGTGCAGGAGACTTGGTCTCAAAG
CTCAGAGAGAGCCAGTCCGGTCCAGCTCCTTTGTCCCTTCTCAGAGGCCTTCTTGAAGATGCATCTAGACT
ACCAGCTTTATCAGTGTTTAAAGTCTTATCTTTTAAACATAAGCTTCTTGACAACATGAATTTGTTGGGTTTTT
GGCGTCTGGTTGACTTTGTTTAGGTTTTGCTTTTATACCCGGGCCAAATAGCACATAACCACTGGTTATATATGAA
TACTCATATGTTTATGACCAAAATAAATATGAAACCTCATRTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 18

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQD
EVPQQTVAPQQQRRSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSG
QTNKSSCTTTTRDTVQCCEKGSFQDKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAA
SSTGKTPAAEETVTTILGMLASPYHYLIIIVVLVIIILAVVVVGFSCRKKFISYLGKICSGGG
GGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQELAELTGVTVES
PEEPQRLLEQAEAEAGCQRRRLLPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKL
FYEEDEAGSATSCL

Important features of the protein:**Transmembrane domains:**

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276,
297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

FIGURE 19

GCGGCACCTGGAAG**ATG**CGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGC**TGA**CACTGCAGGGTCCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAAAAAA

20/75

FIGURE 20

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIKERS

Important features of the protein:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

FIGURE 21

CCGGGGAGGGGAGGGCCCCGTCCCGCCCCCTCCCCGTCTCTCCCCGCCCCCTCCCCGTCCCTCCC
GCCGAAGCTCCGTCCCGCCCCGCGGGCCGGCTCCGCCCTCACCTCCCGGCCGCGGCTGCCCTC
TGCCCGGGTTGTCCAAGATGGAGGGCGCTCCACCGGGGTCGCTCGCCCTCCGGCTCCTGCTG
TTCGTGGCGCTACCCGCCTCCGGCTGGCTGACGACGGGCGCCCCGAGCCGCCGCCGCTGTC
CGGAGCCCCACAGGACGGCATCAGAATTAATGTAACCTACACTGAAAGATGATGGGGACATAT
CTAAACAGCAGGTTGTTCTTAACATAACCTATGAGAGTGGACAGGTGTATGTAAATGACTTA
CCTGTAAATAGTGGTGTAAACCGAATAAGCTGTCAGACTTTGATAGTGAAGAATGAAAATCT
TGAAAATTTGGAGGAAAAAGAATATTTTGGAAATTGTCAGTGTAAGGATTTTAGTTCATGAGT
GGCCTATGACATCTGGTTCCAGTTTGCAACTAATTGTCATTCAAGAAGAGGTAGTAGAGATT
GATGGAAAACAAGTTCAGCAAAAGGATGTCACTGAAATTGATATTTTAGTTAAGAACCGGGG
AGTACTCAGACATTCAAACCTATACCCTCCCTTTGGAAGAAAGCATGCTCTACTCTATTTCTC
GAGACAGTGACATTTTATTTACCCTTCCTAACCTCTCCAAAAAAGAAAGTGTTAGTTCACTG
CAAACCACTAGCCAGTATCTTATCAGGAATGTGGAAACCACTGTAGATGAAGATGTTTTACC
TGGCAAGTTACCTGAAACTCCTCTCAGAGCAGAGCCGCCATCTTCATATAAGGTAATGTGTC
AGTGGATGGAAAAGTTTAGAAAAGATCTGTGTAGGTTCTGGAGCAACGTTTTCCAGTATTC
TTTCAGTTTTTTGAACATCATGGTGGTTGGAATTACAGGAGCAGCTGTGGTAATAACCATCTT
AAAGGTGTTTTTCCCAGTTTCTGAATACAAAGGAATTCTTCAGTTGGATAAAGTGGACGTCA
TACCTGTGACAGCTATCAACTTATATCCAGATGGTCCAGAGAAAAGAGCTGAAAACCTTGAA
GATAAAACATGTATTTAAAACGCCATCTCATATCATGGACTCCGAAGTAGCCTGTTGCCTCC
AAATTTGCCACTTGAATATAATTTTCTTTAAATCGTT

22/75

FIGURE 22

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60783
><subunit 1 of 1, 330 aa, 1 stop
><MW: 36840, pI: 4.84, NX(S/T): 4
MEGAPPGSLALRLLLFVALPASGWLTTGAPEPPPLSGAPQDGIRINVTTLKDDGDISKQQVV
LNITYESGQVYVNDLPVNSGVTRISCQTLIVKNENLENLEEKEYFGIVSVRILVHEWPMTSG
SSLQLIVIQEEVVEIDGKQVQQKDVTEIDILVKNRGVLRHSNYTLPLEESMLYSISRDSIL
FTLPNLSKKESVSSLQTTTSQYLIRNVETTVDVLPGLPETPLRAEPPSSYKVMCQWMEKF
RKDLCRFWSNVFPVFFQFLNIMVVGITGAHVITILKVFFPVSEYKGILQLDKVDVIPVTAI
NLYPDGPPEKRAENLEDKTCI
```

Important features of the protein:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 266-284

Leucine zipper pattern.

amino acids 155-176

N-glycosylation sites.

amino acids 46-49, 64-67, 166-169, 191-194

FIGURE 23

CGTCTCTGCGTTTCGCCATGCGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGG
CCCTGGCTTGGGCGGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGT
GTTTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGTCAC
CCGGGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGG
GGAACAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCACTGCCTTCCCTGCAAAGATTTCG
TGCAGCGGCGTGGAGTGCGGCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCCGCCGCGCTG
CGAGTGCGCGCCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCG
CCACCTACCGCGACGAGTGCGAGCTGCGCGCCGCGCGCTGCCGCGGCCACCCGGACCTGAGC
GTCATGTACCGGGGCGCTGCCGCAAGTCTGTGAGCACGTGGTGTGCCCGCGGCCACAGTC
GTGCGTCTGGACCAGACGGGCAGCGCCCACTGCGTGGTGTGTGAGCGGCGCCCTGCCCTG
TGCCCTCCAGCCCCGGCCAGGAGCTTTGCGGCAACAACAACGTCACCTACATCTCCTCGTGC
CACATGCGCCAGGCCACCTGCTTCCCTGGGCGCTCCATCGGCGTGCGCCACGCGGGCAGCTG
CGCAGGCACCCCTGAGGAGCCGCCAGGTGGTGAGTCTGCAGAAGAGGAAGAGAAGTTCGTGT
GAGCCTGCAGGACAGGCCTGGGCCTGGTGCCCGAGGCCCCCATCATCCCTGTTATTTATT
GCCACAGCAGAGTCTAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTTCGGACCACTT
GGGGATCCCAGAACCTCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGCC
GGCTGGTGGGTGGGATAGACCTGCGTTCCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCT
AGGATGCCCCAGCCCCCTACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTT
TGGGGATAAACCTATTAATTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATT
CCTGAAGAGGCATGACTGCTTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGT
CTAGCCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAG
TACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAG
CCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATG
GAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTG
GGTGAGTATGGAGGGTCTAGCCTGGGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGGA
CCTCAGAACACTGTGACCTTAGCCCAGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGC
CACCATTCCCTGCCAGCCCAAGAACTCCAGCTTCCCCACTGCCTCTGTGTGCCCTTTGCGT
CCTGTGAAGGCCATTGAGAAATGCCAGTGTCGCCCTGGGAAAGGGCACGGCCTGTGCTCC
TGACACGGGCTGTGCTTGGCCACAGAACCACCCAGCGTCTCCCCCTGCTGCTGTCCACGTCAG
TTCATGAGGCAACGTCGCGTGGTCTCAGACGTGGAGCAGCCAGCGGCAGCTCAGAGCAGGGC
ACTGTGTCCGGCGGAGCCAAGTCCACTCTGGGGGAGCTCTGGCGGGGACCACGGGCCACTGC
TCACCCACTGGCCCCGAGGGGGGTGTAGACGCCAAGACTCACGCATGTGTGACATCCGGAGT
CCTGGAGCCGGGTGTCCAGTGGCACCCTAGGTGCCTGCTGCCTCCACAGTGGGGTTTACA
CCCAGGGCTCCTTGGTCCCCCACAACTGCCCGGGCCAGGCCTGCAGACCCAGACTCCAGCC
AGACCTGCCTCACCCACCAATGCAGCCGGGGCTGGCGACACCAGCCAGGTGCTGGTCTTGGG
CCAGTTCTCCACGACGGCTCACCCCTCCCTCCATCTGCGTTGATGCTCAGAATCGCCTACC
TGTGCCTGCGTGTAACACAGCCTCAGACCAGCTATGGGGAGAGGACAACACGGAGGATAT
CCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGCTTGGGCATCCTCCTCCAGCCTCCTC
CAGCCCCCAGGCAGTGCCCTTACCTGTGGTGCCAGAAAAGTGCCCTAGGTTGGTGGGTCTA
CAGGAGCCTCAGCCAGGCAGCCACCCACCCCTGGGGCCCTGCCTCACCAAGGAAATAAAGA
CTCAAGCCATAAAAAAA

24/75

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62306

<subunit 1 of 1, 263 aa, 1 stop

<MW: 27663, pI: 6.77, NX(S/T): 2

MRPGAPGPLWPLPWGALAWAVGFVSSMSGNPAPGGVCWLQQGQEATCSLVLQTDVTRAEC
ASGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGRPRCECAPD
CSGLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCHEHVCPRPQSCVVDQ
TGSAHCVVCRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPE
EPPGGESAEEEEENFV

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

25/75

FIGURE 25

TGCAGAGCTTGTGGAGGCC**ATG**GGGCGCGTCGTGCGGAGCTCGTCTCCTCGCTGCTGGGGT
TGTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGAT
AAAATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAA
ATTTGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGCGCCTGGCTA
CCATGATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTATCCATCCTTTAAATCTG
CACATGAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACT
GGGGATATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGA
TTAAATTAGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTG
TTAGACAAGTTCATGAGGATCTACCGCTACCACTCTCATGACTATGCCTTCAGTAGTGTCGA
AAAATTACTTCATGCTCTAGGAGGAGATGACTTCCTTGGAATGCTTAATCGAACACTTCTTG
AAACCTTGCAAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATG
AGGGTCAATTATGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCACTGTCCTG
TTCTGATTCTGGCCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGC
AGGCATCCAAAAGCAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACC
AAGTACACAGGAAATCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAACCTGAGACTCG
TTCAGACTTCTATGACATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTCGAATATTA
CTTTTCTCAACTTTGATCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACA
ACTTTAGTTAAGGGGGAATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAAATTTGG
CCTTAATACAGTTTTTAACCACTGATAATTCAGATTTGTTTATTAAACAGTATTGGGATTGTGC
CCTCTGTGAGAGAAAAGGAAGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAAGATC
TTTTCCCAAGAACTCTTACTAAAGCACAAATTTTAAAGCTCTTTCTGTCCTATGATTATGC
TGTGAAGAAGCCATGGCTTGCAATATCCTCACTATAAGCCCCCGGAGAAATGCCCTCTATCA
TTCTCCATGATCGACTTTATTACCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATG
AGTGCCATTGCAGCCACAAACGCTGCACTCCTTGCCATATCACCGCTGGAACGGGCACACAGA
CATGATTGATCAGGATGGCTTATATGAGAACTTAAACTGAACTAT**TGA**AGTGACACACTCC
TTTTTCCCCTCCTAGTTCCAAATGACTATCAGTGGCAAAAAGAACAAAATCTGAGCAGAGA
TGATTTTGAACCAGATATTTTGCCATTATCATTGTTTAATAAAAGTAATCCCTGCTGGTCAT
AGGAAAAA

26/75

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880

<subunit 1 of 1, 505 aa, 1 stop

<MW: 56640, pI: 6.10, NX(S/T): 4

MGRVVAELVSSLLGLWLLLCSCGCPEGAELRAPDKIAIIGAGIGGTSAAYYLRQKFGKDVK
IDLFEREEVGGRLATMMVQGGQEYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGE
TLVFEEASNWFIINVIKLVWRYGFQSLRMHMMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHAL
GGDDFLGMLNRTLLETQLQAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLW
AVEGGNKLVCSGLLQASKSNLISGSVMYIEEKTCTKYTGNTKMYEVVYQIGTETRSDFYDI
VLVATPLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFGGLNTVLT
TDNSDLFINSIGIVPSVREKEDPEPSTDGTYYVWKIFSQETLTQAQILKLFLSYDYAVKKPWL
AYPHYKPEKCPSSIILHDRLYYLNIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDG
LYEKLKTEL

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.

amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23, 232-243

27/75

FIGURE 27

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGACATGAT
GCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTG
CAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT
TGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGT
TATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTTGCCCAAATG
AAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACT
GATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTAGACCCTTCTTT
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAGACTTATTCAGTCAGAGCTATAA
GAGATGATGGAAAAAAGCCTTCACTTCAAAGAAGTCAAATTTTCATGAAGAAAACCTCTGGCA
CATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTAAATATTACTATTTAGTTTTTTTA
ATGTGTTTGCAATAGTCTTATTAAAATAAATGTTTTTTTAAATCTGA

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896

<subunit 1 of 1, 166 aa, 1 stop

<MW: 19171, pI: 8.26, NX(S/T): 1

MMLHSALGLCLLLVTVSSNLAIKKEKRPPQTLSRGWGDDITWVQTYEEGLFYAQSKKPL
MVIHHLEDCQYSQALKKVFQAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIMFVDP
SLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL

Important features:**Signal peptide:**

amino acids 1-23

N-myristoylation site.

amino acids 51-57

29/75

FIGURE 29

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGA
AAGAACTGACTGAAACGTTTGAGATGAAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCA
GTGGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAGAAGTATCAGTGACAG
CGATGAATTAGCTTCAGGGTTTTTTTGTGTTCCCTTACCCATATCCATTTTCGCCCACTTCCAC
CAATTCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCT
GCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG
TCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAATTCCTGTTAATAAAAGAAA
AACAAATGTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTA
ATAAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

30/75

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9700, pI: 9.55, NX(S/T): 0

MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPRFP
WFRRNFPIPIPIESAPTTPLPSEK

Important features of the protein:

Signal peptide:

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

FIGURE 31

CGGACGCGTGGGCGGGCGCGCCGGGAGGGACCGGCGGCGGCATGGGCGGGGGCCCTGGGAT
GCGGGCCCGTCTCGCCGCTGCTGCCGCTGTTGCTGCTGCTCGGCCTGGCCCGCGGCGCCGC
GGGAGCGCCGGGCCCCGACGGTTTAGACGTCTGTGCCACTTGCCATGAACATGCCACATGCC
AGCAAAGAGAAGGGAAGAAGATCTGTATTTGCAACTATGGATTTGTAGGGAACGGGAGGACT
CAGTGTGTTGATAAAAATGAGTGCCAGTTTGAGGCCACTCTTGTCTGTGGGAACACACATC
TTGCCACAACACCCCCGGGGGCTTCTATTGCATTTGCCCTGGAAGGATATCGAGCCACAAACA
ACAACAAGACATTTCATTCCCAACGATGGCACCTTTTGTACAGACATAGATGAGTGTGAAGTT
TCTGGCCTGTGCAGGCATGGAGGGCGATGCGTGAACACTCATGGGAGCTTTGAATGCTACTG
TATGGATGGATACTTGCCAAGGAATGGACCTGAACCTTTCCACCCGACCACCGATGCCACAT
CATGCACAGAAATAGACTGTGGTACCCCTCCTGAGGTTCCAGATGGCTATATCATAGGAAAT
TATACGTCTAGTCTGGGCAGCCAGGTTCTGTTATGCTTGCAGAGAAGGATTCTTCAGTGTTCC
AGAAGATACAGTTTCAAGCTGCACAGGCCTGGGCACATGGGAGTCCCCAAAATTACATTGCC
AAGAGATCAACTGTGGCAACCCTCCAGAAATGCGGCACGCCATCTTGGTAGGAAATCACAGC
TCCAGGCTGGGCGGTGTGGCTCGCTATGTCTGTCAAGAGGGCTTTGAGAGCCCTGGAGGAAA
GATCACTTCTGTTTGCACAGAGAAAGGCACCTGGAGAGAAAGTACTTTAACATGCACAGAAA
TTCTGACAAAGATTAATGATGTATCACTGTTTAAATGATACCTGTGTGAGATGGCAAATAAAC
TCAAGAAGAATAAAACCCCAAGATCTCATATGTGATATCCATAAAAGGACAACGGTTGGACCC
TATGGAATCAGTTCGTGAGGAGACAGTCAACTTGACCACAGACAGCAGGACCCCAAGAGTGT
GCCTAGCCCTGTACCCAGGCACCAACTACACCGTGAACATCTCCACAGCACCTCCCAGGCGC
TCGATGCCAGCCGTCATCGGTTTCCAGACAGCTGAAGTTGATCTCTTAGAAGATGATGGAAG
TTTCAATATTTCAATATTTAATGAAACTTGTTTGAATGAACAGGCGTTCTAGGAAAGTTG
GATCAGAACACATGTACCAATTTACCGTTCTGGGTGAGAGGTGGTATCTGGCTAACTTTTCT
CATGCAACATCGTTTAACTTCACAACGAGGGAACAAGTGCCTGTAGTGTGTTTGGATCTGTA
CCCTACGACTGATTATACGGTGAATGTGACCCTGCTGAGATCTCCTAAGCGGCACTCAGTGC
AAATAACAATAGCAACTCCCCCAGCAGTAAACAGACCATCAGTAACATTTTCAGGATTTAAT
GAAACCTGCTTGAGATGGAGAAGCATCAAGACAGCTGATATGGAGGAGATGTATTTATTCCA
CATTTGGGGCCAGAGATGGTATCAGAAGGAATTTGCCCCAGGAAATGACCTTTAATATCAGTA
GCAGCAGCCGAGATCCCGAGGTGTGCTTGACCTACGTCCGGGTACCAACTACAATGTCACT
CTCCGGGCTCTGTCTTCGGAACCTTCTGTGGTCACTCTCCCTGACAACCCAGATAACAGAGCC
TCCCCCTCCCGGAAGTAGAATTTTTTACGGTGCACAGAGGACCTCTACCACGCCTCAGACTGA
GGAAAGCCAAGGAGAAAAATGGACCAATCAGTTCATATCAGGTGTTAGTGCTTCCCCTGGCC
CTCCAAAGCACATTTTCTTGTGATTCTGAAGGCGCTTCCCTCCTTCTTTAGCAACGCCTCTGA
TGCTGATGGATACGTGGCTGCAGAACTACTGGCCAAAGATGTTCCAGATGATGCCATGGAGA
TACCTATAGGAGACAGGCTGTACTATGGGGAATATTATAATGCACCCTTGAAAAGAGGGAGT
GATTACTGCATTATATTACGAATCACAAGTGAATGGAATAAGGTGAGAAGACACTCCTGTGC
AGTTTGGGCTCAGGTGAAAGATTCTGTCACCTCATGCTGCTGCAGATGGCGGGTGTGGACTGG
GTTCCCTGGCTGTTGTGATCATTCTCACATTCCTCTCCTTCTCAGCGGTGTCATGGCAGATG
GACACTGAGTGGGGAGGATGCACTGCTGCTGGGCAGGTGTTCTGGCAGCTTCTCAGGTGCC
GCACAGAGGCTCCGTGTGACTTCCGTCCAGGGAGCATGTGGGCCTGCAACTTTCTCCATTCC
CAGCTGGGCCCCATTCTGGATTTAAGATGGTGGCTATCCCTGAGGAGTCACCATAAGGAGA
AACTCAGGAATTCTGAGTCTTCCCTGCTACAGGACCAGTTCCTGTGCAATGAACTTGAGACT
CCTGATGTACACTGTGATATTGACCGAAGGCTACATACAGATCTGTGAATCTTGGCTGGGAC
TTCTCTGAGTGATGCCTGAGGGTCAGCTCCTCTAGACATTGACTGCAAGAGAATCTCTGCA
ACCTCCTATATAAAAGCATTTCTGTTAATTCATTGAGAATCCATTCTTTACAATATGCAGTG
AGATGGGCTTAAGTTTGGGCTAGAGTTTGACTTTATGAAGGAGGTGATTGAAAAGAGAACA
GTGACGTAGGCAAATGTTTCAAGCACTTTAGAAACAGTACTTTTCTATAATTAGTTGATAT
ACTAATGAGAAAATATACTAGCCTGGCCATGCCAATAAGTTTCTGCTGTGTCTGTTAGGCA
GCATTGCTTTGATGCAATTTCTATTGTCTTATATATTCAAAGTAATGTCTACATTCCAGTA
AAAATATCCCGTAATTAAAAA

33/75

FIGURE 33

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
GGCTGTCTCTGGGGTCTGGCTCTGCCCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
GAGCTCTGCAGGCCCCAGCACCCGCAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCAGAAAGCAGAGACCAGGGGAGCCAA
GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTG
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGCACCGA
TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAGCTAAGGGCCTGTCCTCAGAGAGCAGTGCCCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT
GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTACAAACATCGAG
GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACTTCCAGCATCCCTGGGGCCTCAGA
CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTCACAGCCTCTGCCGAGACCCTGTCC
ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGAGCTCTGGTCA
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTTC
CTTTGCTGGGAGCTCTGCTTCTCCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGGCCCTTCCCCACCAGCAGGGACCCCT
CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCACGACTGCCCGGAC
GAGGCCGACCACAGACG**TGA**GTGCAGGTGAAAATGGAGGTTTCCTCCTCCTGCGGCTGAGTG
TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
CGGGAACCTCCACGCCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTCAGGAGAGGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCCCTAGCCTG
GGCCCCCACCAGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC
CGGAGTGTATGTATGGGGAGGGGCTTCACCTGTTCCAGAGGTGTCCTTGGACTCACCTTGG
CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
TTAAAATTCACTCAGTGTGGCCCAAAAAAA

34/75

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108722

><subunit 1 of 1, 482 aa, 1 stop

><MW: 49060, pI: 4.74, NX(S/T): 4

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTKTSPNFMVLIATSVETSAASGSPEGAGM
 TTVQITITGSDPEEAIFDTLCTDDSSSEEAKTLTMDILTTLAHTSTEAKGLSSESSASSD
 GPHPVITPSRASESSASSDGPVITPSRASESSASSDGPVITPSWSPGSDVTLLEALVT
 VTNIEVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEV
 TASAETLSTAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETS
 ALSVETPSYVKVSGAAPVSIIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPT
 MDIATKGPFPPTSRLPLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRPRLPGR
 GRPQT

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-88

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284,
 314-320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 35

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAG
GCC**ATG**CCTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCCTGTTAATTCTGGCTTTGGGCCA
GGCAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCAC
CCCAGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTTCCAGGATCGCGAGGCAGCA
GCGACCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGT
ACTTCGCTTTCTCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCT
CCTGCCTGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACA
TTGGCCCAGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGA
ACTGGCTCTGTTCTGGTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTA
AAATGTTTGTGTTGCGGTCAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGAT
GTAGCTAAGGATTGGAATGACAACCCCCGGAAAAATTTCTGGGTATTCTTGGAGATACTGGT
CAAAGAAGATAGAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGAT
GCTCCCTTCATGCTTCCCTGCTGGTGGTGACTCTCAACCCTGATCAGTGCCACCCTTCTCGG
AAAAGGAGAGCAGCCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCTCTGCCACCGTCACCA
GCTATTCATTAACTTCCGGGACCTGGGTGGCACAAGTGATCATTGCCCCCAAGGGGTTC
TGGCAAATTACTGCCATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAAT
TATGCTTTCATGCAAGCCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTAT
CCCCACCAAGCTGTCTCCCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTAC
GACATTATGAAGACATGGTAGTCGATGAATGTGGGTGTGGG**TAG**GATGTCAGAAATGGGAAT
AGAAGGAGTGTTCTTAGGGTAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTA
GATCGAAATGTC

36/75

FIGURE 36

MLRFLPDLAFSFLLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQPVPIYLKKIFQDREAAA
 TTGVSRDLCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTL
 AQLGLDLGPNSYYNLGPELELALFLVQEPHVWGQTTPKPGKMFVLRSPWPQGAVHFNLLDV
 AKDWNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRK
 RRAAIPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPCHGECPFSLTISLNSSNY
 AFMQALMHAVDPEIPQAVCIPTKLSPISMLYQDNNDNVILRHYEDMVVDECGCG

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

FIGURE 37

CAC TTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTTCGCAGAGAC
CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCTGCTCTGTT
TCCTTACCCGAGTCTGTGCATCGCCCCGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
TGCTCTAGGGGGCGCGCGGGAGGAGCGGCCGGGACGGAGGGCCCGGCAGGAAGATGGGC
TCCCGTGGACAGGGACTCTTGTGGCGTACTGCCTGCTCCTTGCCTTTGCCTCTGGCCTGGT
CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG
GACCAGGGGGCTCCCTGCTTCCCGGTGCTTGCCTGCTGTGACCCCGGTACCTCCATGTACCC
GGCGACCGCGCTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG
ATCGAGGCCTCCAAGGGAAATATGGCAAACAGGCTCAGCAGGGGGCCAGGGGCCACACTGGA
CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTTCGGTGGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG
ACACGGAGTTTCGTGAACCTCTACGACCACTTCAACATGTTACCGGCAAGTTCTACTGCTAC
GTGCCCCGGCCTCTACTTCTTCAGCCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTGGGCGACCGCAGCA
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC
TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG
TGGCTACCTGGTCAAGCACGCCACCGAGCCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCC
ACCTTCCACCCCTGCGCTGTGCTGACCCCAACCGCTCTTCCCGATCCCTGGACTCCGACTC
CCTGGCTTTGGCATTTCAGTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC
GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC
GAGACGCGGGTGGCGGCAGGGCGTCCCAGGGTGGCGCACCGCGGCTCCAGTCTTGGAATA
ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
TTGTTATTTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCTTTTCAGTTGAG
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGGCCGGGGGAGG
AAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTCTTGAGGGATAGGTGGACC
CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT
GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA
GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
ACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATGCCCTGCCACCTGGCATCGGCT
TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCTTCTGTTTTT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTCGTGGGCTAAGCATCACCGCTT
CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCT
CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG
CTGGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCTTG
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTCAGGATTCAGTCTCAGGAGC
TGGGTGGCAGGAGAGGCAATAGCCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG
GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCC
ATAGCCCCCTCTCCACCTCACCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCC
CCCAAACCCCGCTGCCTCTCTTCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGC
TTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACATC
GCTGCTTAAGCTCCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

38/75

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAI FSEELDTYITFSGYLVKHATEP
```

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 39

GAATTCGGCACGAGGGAAGAAGAGAAAGAAAATCTCCGGGGCTGCTGGGAGCATATAAAGAA
GCCCTGTGGCCTTGCTGGTTTTACCATCCAGACCAGAGTCAGGCCACAGACGGAC**ATG**GCTG
CTCAAGGCTGGTCCATGCTCCTGCTGGCTGTCCTTAACCTAGGCATCTTCGTCCGTCCCTGT
GACACTCAAGAGCTACGATGTCTGTGTATTTCAGGAACACTCTGAATTCATTCCTCTCAAAC
CATTAAAAATATAATGGTGATATTCGAGACCATTTACTGCAACAGAAAGGAAGTGATAGCAG
TCCCAAAAAATGGGAGTATGATTTGTTTGGATCCTGATGCTCCATGGGTGAAGGCTACTGTT
GGCCAATTACTAACAGGTTCCCTACCTGAGGACCTCAAACAAAAGGAATTTCCACCGGCAAT
GAAGCTTCTGTATAGTGTTGAGCATGAAAAGCCTCTATATCTTTCATTTGGGAGACCTGAGA
ACAAGAGAATATTTCCCTTTCCAATTCGGGAGACCTCTAGACACTTTGCTGATTTAGCTCAC
AACAGTGATAGGAATTTTCTACGGGACTCCAGTGAAGTCAGCTTGACAGGCAGTGATGCCT**TA**
AAAGCCACTCATGAGGCAAAGAGTTTCAAGGAAGCTCTCCTCCTGGAGTTTTGGCGTTCTCA
TTCTTATACTCTATTCCCGCGTTAGTCTGGTGTATGGATCTATGAGCTCTCTTTTAATATTT
TATTATAAATGTTTTATTTACTTAACTTCCTAGTGAATGTTACAGGTGACTGCTCCCCCAT
CCCCATTTCTTGATATTACATATAATGGCATCATATAACCCCTTTATTGACTGACAAACTACT
CAGATTGCTTAACATTTTGTGCTTCAAAGTCTTATCCCACTCCACTATGGGCTGTTACAGAG
TGCATCTCGGTGTAGAGCAAGGCTCCTTGTCTTCAGTGCCCCAGGGTGAAATACTTCTTTGA
AAAATTTTCATTCATCAGAAAATCTGAAATAAAAATATGTCTTAATTGAG

40/75

FIGURE 40

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73838
><subunit 1 of 1, 167 aa, 1 stop
><MW: 19091, pI: 7.48, NX(S/T): 1
MAAQGWSMLLLAVLNLGIFVRPCDTQELRCLCIQEHSEFIPLKLIKIMVIFETIYCNRKEV
IAVPKNGSMICLDPDAPWVKATVGPITNRFLPEDLKQKEFPFAMKLLYSVEHEKPLYLSFGR
PENKRIFPFPIRETSRHFADLAHNSDRNFLRDSSEVSLTGSDA
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 68-72

N-myristoylation site.

amino acids 69-75

Small cytokines (intercrine/chemokine) C-x-C subfamily signature

amino acids 40-85

41/75

FIGURE 41

CAGACATGGCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGGCATCCCC
AGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCAAGTACAGCCAAAGGAAGAT
TCCCGCCAAGGTTGTCCGCAGCTACCGGAAGCAGGAACCAAGCTTAGGCTGCTCCATCCCAG
CTATCCTGTTCTTGCCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTC
TGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAACCAGCCCAGGG
CTGCAGGAAGGACAGGGGGGCTCCAAGACTGGCAAGAAAGGAAAGGGCTCCAAAGGCTGCA
AGAGGACTGAGCGGTCACAGACCCCTAAAGGGCCATAGCCCAGTGAGCAGCCTGGAGCCCTG
GAGACCCACACAGCCTCACCAGCGCTTGAAGCCTGAACCCAAGATGCAAGAAGGAGGCTATG
CTCAGGGGCCCTGGAGCAGCCACCCCATGCTGGCCTTGCCACACTCTTTCTCCTGCTTTAAC
CACCCCATCTGCATTCCCAGCTCTACCCTGCATGGCTGAGCTGCCCACAGCAGGCCAGGTCC
AGAGAGACCGAGGAGGGAGAGTCTCCCAGGGAGCATGAGAGGAGGCAGCAGGACTGTCCCT
TGAAGGAGAATCATCAGGACCCTGGACCTGATACGGCTCCCCAGTACACCCACCTCTTCCT
TGTAATATGATTTATACCTAACTGAATAAAAAGCTGTTCTGTCTTCCNCCCCA

42/75

FIGURE 42

><MW: 14646, pI: 10.45, NX(S/T): 0

MAQSLALSLILVLAFGIPTQGS DGG AQDCCLKYSQRKIPAKVVRSYRKQEPSLGCSIPAI
LFLPRKRSQAELCADPKELWVQQLMQHLDKTPSPQKPAQGCRKDRGASKTGKKGKGSKGCKR
TERSQTPKGP

Important features of the protein:

Signal peptide:

amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 67-71

N-myristoylation sites.

amino acids 17-23, 23-29, 27-33, 108-114, 118-124, 121-127

Amidation site.

amino acids 112-116

Small cytokines.

amino acids 51-91

FIGURE 43

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC
 CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
 CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
 ACACCTTCCCAAATGTCACCTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
 GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
 TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
 TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
 AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
 ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
 CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
 GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
 CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
 TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
 CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
 GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCATATTTTACCTATGA

FIGURE 44

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA
```

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 45

GCTCCCAGCCAAGAACCTCGGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
 CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCGGCTGGGA
 CAAGAAGCCGCCGCTGCCTGCCCGGGCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG
 GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
 TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG
 CCGCCGCGCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
 GGCACCTCACAGCCCCGCGAGCGCATCCCGGTGCGCGCCCGAGCCTCCCGCACCCCCATCGCCGG
 AGCTGCGCCGAGAGCCCCAGGGAGGTGCC**ATG**CGGAGCGGGTGTGTGGTGGTCCACGTATGG
 ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
 CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC
 ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGGACTGCGCGCGGGGC
 CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
 CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
 ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA
 TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
 CAGAGGCTTTCTTCCACTCTCTCATTTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
 AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGCATG
 GACCCATTTGGGCTTGTCACCGGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAG**TAA**CT
 GAGACCATGCCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
 TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
 GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
 CATAACATTGTAAGCCTGTAGCTTGCCCAGCTGCTGCCTGGGCCCCCATTTCTGCTCCCTCGA
 GGTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
 TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC
 CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTACAGGAACAGGTGATCCACTCTGTA
 AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
 ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAG
 GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCC
 CTGAGGCCAGTTCTGTCTATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACTGC
 TTCCATCTCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT
 CCCAGGCCCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
 TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
 CCTTTCCCCAGCACTTGGTTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
 TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAGGTTTG
 TTTTGTATATTAAATGGAGTTTGTTTGT

FIGURE 46

MRSGCVVHVHVLWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
 RADGVVDCARGQSAHSLLEIKAVALLRTVAIKGVHVSRYLCMGADGKMQGLLQYSEEDCAFEE
 EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
 MFSSPLETDSMDPFGGLVTGLEAVRSPSEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

47/75

FIGURE 47

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACCTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTCAATCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAAT
CTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTTCCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACCTGTTTTAA
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGGTCGCAGGAATCTGCACTCAACTGCCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTTCTGGGCTCTTTCCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTTCGGGATCAGCCTGACCA
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

FIGURE 48

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTRRLVCYNNKITASYEDRVTFLLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

[illegible]

FIGURE 50

MGAARLLPNLTLCLQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLGKPSGKSKDCVFTEIVLE
NNYTAFQNARHEGWFMATRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

51/75

FIGURE 51

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACC GAACCTGACAAAAAAGAAGAAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATA
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAAC TACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

52/75

FIGURE 52

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYEC SASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGT LQCEASAV
PSAEFQWYKDDKRLIEGKKG VKVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGH TNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

Signal peptide:

amino acids 1-28

[illegible]

54/75

FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLALLCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSSGGSSSSGSSSSGSSSSGSSSGGSSSGGSSSGNSGGSRGDSGSESSW
GSSTGSSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
GGSGDNRYRGQSSWGSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 55

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATG**GCAAT
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATG
AAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGGCCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACCTGAC
AAATGCAACGCCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCACCGAGGGCACCACCAGCCCCCTGGACAGCCATCGACCTCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGC
ATAGACCGCCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

56/75

FIGURE 56

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTILVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAPHLMTDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFSVPVYIRTCHR
PSCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVG
LSA

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

57/75

FIGURE 57

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGT**TGAT**GAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTGAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

58/75

FIGURE 58

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
 SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
 SCSVNVQDKQGKSRGHSIKTLELNVLPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
 WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
 VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
 SSVTSARALRPPHGP RP PGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
 MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
 262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 59

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAAGAGGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
 CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
 CATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT
 TTCCGTACTTCAGAA**ATG**GGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCCCT
 GAAGTCTTGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
 CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
 CCTCTTGCGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC
 TGGATTTCTGTCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
 AACTGGACGAATTCCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAC
 AATATTCAGACCATTTACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGGCTATTAGCC
 TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCCCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCATATCCGACATGGCCTTCCAGAA
 TCTCACGAGCTTGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
 AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC
 CACCCTCCTCCCGATCTCCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT
 AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
 ACTGCTCGGAATAACCCCTTGGTTTTGTGACTGCAGTATTAATGGGTACAGAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTGAACAAGTCCGGG
 GGATGGCCGTCAGGGAATTAAATATGAATCTTTTGTCTGTCCCACCACGACCCCCGGCCTG
 CCTCTCTTACCCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT
 TCCAAACCCTAGCAGAAGCTACACGCCTCCAACTCCTACCACATCGAAACTTCCCACGATTC
 CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCGTGATGGCATA
 CAAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG
 TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
 TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGC
 CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
 CGTCCCACAGCATGGGCTCCCCCTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
 GTGCTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAGGGGCGCTACACCTC
 CCAGAAGTGGAATAACAACCGGGGGCGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
 AGGACAACCTCCATCCTGGAGATGACAGAAACAGTTTTCAGATCGTCTCCTTAAATAACGAT
 CAACTCCTTAAAGGAGATTTTCACTGACAGCCCATTACACCCCAAATGGGGGCATTAATTA
 CACAGACTGCCATATCCCCAACAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
 ACTGCCATACG**TGA**CAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
 CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
 TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
 CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACCTCTTTGCTTTTTTAAATCTT

amino acids 39-50

FIGURE 61

TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAACTGTTATTTACTGCTGCGTTT
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA
AAGTCAAGCAGCCAGTGCATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
CAATGGAAACAATTCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAACAACAAGTGTATTAATTAACCTTTCAGATGTAAATGACAATAAGCCTATATTTAA
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
GATTCGCAAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTTAA
AAAGAAAGTGGATTTTGGAGCACCAGAACCACTACGGTATTAGAGCAAAGTTAAAAACCATC
ATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAGATCCAG
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTTGA
AGAAACCCACAGGGATCATTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCATATCAATGATAATGGTACAATC
ACTACAAGTAACCTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATCA
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAGTTTTACAATCATAGATAATCAAG
ATAACACAGCTGTCATTTTGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTCATTATGATCATA
TTTGGGTTTATTTTTTTGACTTTGGGTTTAAACAACGGAGAAAACAGATTCTATTTCTGA
GAAAAGTGAAGATTTTCAAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
CAGTGCCATATTCAAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
CCCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGCTTCTGCAGTGCAGTCAAATAATTAGG
GCTTTTTTACCATCAAAATTTTTTAAAAGTGCTAATGTGTATTGCAACCAATGGTAGTCTTAA
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC
CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTCATTGAACAGAGATGTG
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAAACAGATTTGAAGTAAATAATG
TAGGAAAGTATTAAGAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
CATTATTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCCATGAAGTATTGTTTCCTTTAT
TTAAA

62/75

FIGURE 62

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSL LQGQPYFSVEPTTG VIRISSKMDRELQDEYWV I IQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEEHHFYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVCD CGDSGSTQTCQYQELVLSMGFKTEV I IAILICIM I IFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPD SAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLES AVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN
```

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

63/75

FIGURE 63

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGC
CGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTC
TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCAGTGCAGGCTTGAC
AAGTCCAACCTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAG
CTTGGCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTA
TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTT
CCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAG
CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAA
AGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAAGTG
GATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAA
TAACTAACCCCTTTCCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAAC
CAAAAGGAAGATGGGAAGCCAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGT
TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCA
TAGATATTTATTGATAACATTTTATTGTAAGTGGTGTCTATACACAGAAAACAATTTATTT
TTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCATTCCTTTAGGGGAAAAAACCC
CTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTA
TAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCG
ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAAC
ATGTTTATTTGACCTCAATAAACACTTGGATATCCC

64/75

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125185

><subunit 1 of 1, 179 aa, 1 stop

><MW: 20011, pI: 8.10, NX(S/T): 3

MAALQKSVSSFLMGTLATSCLLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKE
ASLADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVPFLAR
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 65

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCCCTCCGGCTGCGAGAAAGGA
CGCGCGCCCTGCGTCGGGCGAAGAAAAGAAGCAAACTTGTCTGGGAGGGTTTCGTCAACA
CTCCTTCCCGCAAACCTAAACCTCCTGCCGGGGCCATCCCTAGACAGAGGAAAGTTCCTGCA
GAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGCGCTGGCTGTGGAATTAGATCTGT
TTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGCACC GGTTGG
CGCTGCCCCGAGTGGAAACCGACAGTTTGCGAGCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCG
GTTGTTGTTTCAAGTGTCTGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGG
TCCGAAGAGCGCTGCGCTCCTACTCGCGTTCTGCTTCTTCTCTCTCGGTTCCCTACTGTGA
AATCGCAGCGACATTTACAAAGGCCTCCGGGTCTTACCGAGACCGATCCGCAGCGTTTGGCC
CGGTCTGTGCTATTGCATCGGGAGCCCCCGAGCACCGGCGAAATGCGGAGGGTCCC GAAGGC
CGACCTGGCCGCTGCAGGAGTTATGTTACTTTGCCACTTCTTCACGGACCAGTTTCAGTTTCG
CCGATGGGAAACCCGGAGACCAATCCTTGATTGGCAGTATGGAGTTACTCAGGCCTTCCCT
CACACAGAGGAGGAGGTGGAAGTTGATTCACACGCGTACAGCCACAGGTGGAAAAGAACTT
GGACTTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGAGCCCA
GAAGCTTCACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGAT
ACAGACCACAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTT
ATGGGTGAACATAGACCAATGGAAAAAGATAAAGTGAAGATTCATGGAATATTGTCCAATA
CTCATCGGCAAGCTGCAAGAGTGAATCTGTCTTTCGATTTTCCATTTTATGGCCACTTCCTA
CGTGAAATCACTGTGGCAACCGGGGGTTCATATACACTGGAGAAGTCGTACATCGAATGCT
AACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCCAGTGTATCCAGAAATT
CAACTGTCAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTC
CAGGATAATTATAACCTGGGAAGCTTCACATTCCAGGCAACCCCTGCTCATGGATGGACGAAT
CATCTTTGGATACAAAGAAATTCCTGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAG
TGAAAGTCGGACTGTCCGATGCATTTGTCTGTTGTCCACAGGATCCAACAAATTTCCCAATGTT
CGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAAAATTACCAACAT
TTCGGCTGTGGAGATGACCCCATTAACCCACATGCCTCCAGTTTAAACAGATGTGGCCCTGTG
TATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAACTTCAAAGATGTTCCAGTGGGA
TTTGATCGTCATCGGCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAGAGAGAAGAT
GTGTGAGAATACAGAACCAGTGGAAACTTCTTCTCGAACCACCACAACCGTAGGAGCGACAA
CCACCCAGTTCAGGGTCCTAACTACCACCAGAAGAGCAGTGACTTCTCAGTTTCCCACCAGC
CTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGCTTCTACAGA
TGACAGTGCAGCTGAGAAGAAAGGGGGAACCCCTCCACGCTGGCCTCATCATTGGAATCCTCA
TCCTGGTCTTCATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAACA
TCAGCAGCCAGCATCTTCTTTATTGAGAGACGCCCAAGCAGATGGCCTGCGATGAAGTTTAG
AAGAGGCTCTGGACATCCTGCCTATGCTGAAGTTGAACCAGTTGGAGAGAAAGAAGGCTTTA
TTGTATCAGAGCAGTGCTTAAATTTCTAGGACAGAACAACACCAGTACTGGTTTACAGGTGT
TAAGACTAAAATTTTGCCTATACCTTTAAGACAAACAAACACACACACAAACAAGCTC
TAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGG
TAAACAAAAAACTAAACTTATACAAGATACCATTTTACTGAACATAGAATTCCCTAGTGG
AATGTCATCTATAGTTCCTCGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTA
TAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAGGGATCAGAAAAAAAATCATAATAAAGC
TTTAGTTCATGAGGG

FIGURE 66

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVGTQAFPHTEEEVEVD SHAYS
HRWKRNLDLFLKAVDTNRSVQGDSPEPRSFTDLLLDDGQDNNTQIEEDTDHNYYSISRIYGPS
DSASRDLWVNIDQMEKDKVKI HGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTG
EUVHRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQAT
LLMDGRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFV VVHRIQQIPNVRRRTIYEYHRVELQ
MSKITNISAVEMTPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCP
EESKEKMCENTEPVETSSRTTTTVGATTTQFRVLTTT RRAVTSQFPTSLPTEDDTKIALHLK
DNGASTDDSAAEKKGGTLHAGLIIGILILVLIVATAILVTVMYHHPTSAASIFFIERRPSR
WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.

amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

67/75

FIGURE 67A

GCAGCCCTAGCAGGGATGGACATGATGCTGTTGGTGCAGGGTGCCTTGTTGCTCGAACCAGTG
GCTGGCGGCGGTGCTCCTCAGCCTGTGCTGCCTGCTACCCCTCCTGCCTCCCGGCTGGACAGA
GTGTGGACTTCCCCTGGGCGGCCGTGGACAACATGATGGTCAGAAAAGGGGACACGGCGGTG
CTTAGGTGTTATTTGGAAGATGGAGCTTCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTAT
TTTTGCGGGAGGTGATAAGTGGTCAGTGGATCCTCGAGTTTCAATTTCAACATTGAATAAAA
GGGACTACAGCCTCCAGATACAGAATGTAGATGTGACAGATGATGGCCCATACACGTGTTCT
GTTCACTCAACATACACCCAGAACAATGCAGGTGCATCTAACTGTGCAAGTTCTCTCTAA
GATATATGACATCTCAAATGATATGACCGTCAATGAAGGAACCAACGTCACTCTTACTTGTT
TGGCCACTGGGAAACCAGAGCCTTCCATTTCTTGGCGACACATCTCCCCATCAGCAAAACCA
TTTGAAAATGGACAATATTTGGACATTTATGGAATTACAAGGGACCAGGCTGGGGAATATGA
ATGCAGTGCAGAAAATGATGTGTCATTCCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACT
TTGCTCCTACTATTTCAGGAAATTAATCTGGCACCGTGACCCCGGACGCAGTGGCCTGATA
AGATGTGAAGGTGCAGGTGTGCCGCCTCCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCT
CTTCAATGGCCAACAAGGAATTATTATTCAAATTTTAGCACAAGATCCATTCTCACTGTTA
CCAACGTGACACAGGAGCACTTCGGCAATTATACTTGTGTGGCTGCCAACAAGCTAGGCACA
ACCAATGCGAGCCTGCCCTCTTAACCCTCCAAGTACAGCCCAGTATGGAATTACCGGGAGCGC
TGATGTTCTTTTCTCCTGCTGGTACCTTGTGTTGACACTGTCCTCTTTCACCAGCATATTCT
ACCTGAAGAATGCCATTCTACAATAAATTCAAAGACCCATAAAAAGGCTTTTAAGGATTCTCT
GAAAGTGCTGATGGCTGGATCCAATCTGGTACAGTTTGTAAAGCAGCGTGGGATATAATC
AGCAGTGCTTACATGGGGATGATCGCCTTCTGTAGAATTGCTCATTATGTAAATACTTTAAT
TCTACTCTTTTTTGTATTAGCTACATTACCTTGTGAAGCAGTACACATTGTCCTTTTTTTAAG
ACGTGAAAGCTCTGAAATTACTTTTAGAGGATATTAATTGTGATTTTCATGTTTGTAATCTAC
AACTTTTCAAAGCATTTCAGTCATGGTCTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAA
TATTGCAGTGAATATGTGATTCTTTAAGGCTGCAATACAAGCATTTCAGTTCCCTGTTTCAAT
AAGAGTCAATCCACATTTACAAAGATGCATTTTTTTCTTTTTTGATAAAAAAGCAAATAATA
TTGCCTTCAGATTATTTCTTCAAATATAACACATATCTAGATTTTTCTGCTCGCATGATAT
TCAGGTTTCAGGAATGAGCCTTGTAATATAACTGGCTGTGCAGCTCTGCTTCTCTTCTGT
AAGTTCAGCATGGGTGTGCCTTCATACAATAATTTTTCTCTTTGTCTCCAATAATATAA
AATGTTTTGCTAAATCTTACAATTTGAAAGTAAAAATAAACCAGAGTGATCAAGTTAAACCA
TACACTATCTCTAAGTAACGAAGGAGCTATTGGACTGTAAAAATCTCTTCTGCACTGACAA
TGGGGTTTGAGAATTTTGCCCCACACTAACTCAGTTCTTGTGATGAGAGACAATTTAATAAC
AGTATAGTAAATATACCATATGATTTCTTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGA
AATCATTTCCCTTTAAATGACAGCACAGTCCACTCAAAGGATTGCCTAGCAATACAGCATCT
TTTCTTTCACTAGTCCAAGCCAAAAATTTAAGATGATTTGTGAGAAAGGGCACAAAGTCC
TATCACCTAATATTACAAGAGTTGGTAAGCGCTCATCATTAAATTTTATTTTGTGGCAGCTAA
GTTAGTATGACAGAGGCAGTGCTCCTGTGGACAGGAGCATTTTGCATATTTTCCATCTGAAA
GTATCACTCAGTTGATAGTCTGGAATGCATGTTATATATTTTAAACTTCCAAAATATATTA
TAACAAACATTCTATATCGGTATGTAGCAGACCAATCTCTAAAATAGCTAATTCTTCAATAA
AATCTTTCTATATAGCCATTTTCAGTGCAACAAGTAAAATCAAAAAAGACCATCTTTATTT
TTCCTTACATGATATATGTAAGATGCGATCAAATAAAGACAAAACACCAGTGATGAGAATAT
CTTAAGATAAGTAATTATCAAATTATTGTGAATGTTAAATTATTTCTACTATAAAGAAGCAA
AACTACATTTTGAAGGAAAATGCTGTTACTCTAACATTAATTTACAGGAATAGTTTGATGG
TTTCACTCTTTACTAAAGAAAGGCCATCACCTTGAAAGCCATTTTACAGGTTTGATGAAGTT
ACCAATTTACAGTACACCTAAATTTCTACAAATAGTCCCCTTTTACAAGTTGTAACAACAAAG
ACCTATAATAAAATAGATACAAGAAATTTTGAGTGTTTATACATATTTGAGATATCTAG
TATGTTGCCCTAGCAGGGATGGCTTAAAAACTGTGATTTTTTTTTCTTCAAGTAAAACCTAGT
CCCAAAGTACATCATAAATCAATTTTAATTAGAAAAATGAATCTTAAATGAGGGGACATAAG
TATACTCTTTCCACAAAATGGCAATAATAAGGCATAAAGCTAGTAAATCTACTAACTGTAAT
AAATGTATGACATTATTTTGATTGATACATTAAAAAGAGTTTTTTAGAACAAATATGGCATT
TAACCTTTATTATTTATTTGCTTTTAAAGAAATATTCTTTGTGGAATTGTTGAATAAACTATAA
AATATTATTTTGTATTGCAGCTTTAAAGTGGCACACTCCATAATAATCTACTACTAGAAAT

FIGURE 67B

AGTGGTGCTACCACAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAGAAACAGATC
AAGAATGCATATTATTTCAGTGACCGCTTTCCTAGAGTTAAAATACCTCCTCTTTGTAAGGTT
TGTAAGGTAAATTGAGGTATAAACTATGGATGAACCAAATAATTAGTTCAAAGTGTTGTCATG
ATTCCAAATTTGTGGAGTCTGGTGTTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT
CAGTAGCTATATGTATTTGCCTTTATGTTAGAAGAGACTTTCCTTGAGTGACATTTTTTAAATA
GAGGAGGTATTCACATATGTTTTTCTGTATCACAGCAGCATTCCTAGTCCTTAGGCCCTCGGA
CAGAGTGAAATCATGAGTATTTATGAGTTCAATATTGTCAAATAAGGCTACAGTATTTGCTT
TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTATGGACATATAA
AATGTCTGATTACCCCATTTTATCAGTCCTGACTGTACAAGATTGTTGCAATTTCAGAATAG
CAGTTTTATAAATTGATTTATCTTTTAATCTATAACAATTTGTGTTAGCTGTTTCATTTTCAGG
ANTATATTTTCTACAAGTTCCTTGTGGGACTCCTTTTGTGCCCCCTATTTTTTTTTTAAAG
AAGGAAGAAAGAAAAATAAGTAGCAGTTTAAAAATGAGAATGGAGAGAAAAGAAAAAGAATG
AAAAGGAAAGGCAGTAAAGAGGGAAAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG
AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGAAGGAAGAATCAGAGTATTAGG
GTAGTTAACTTACACATTTGCATTCTTAGTTTTAACTGCAAGTGGTGTAAGTATGTTTTTCAA
TGATCGCATTTGAAACATAAGTCCTATTATACCATTAAAGTTCCTATTATGCAGCAATTATAT
AATAAAAAGTACTGCCCAAGTTATAGTAATGTGGGTGTTTTTGAGACACTAAAAGATTTGAG
AGGGAGAATTTCAAACCTTAAAGCCACTTTTGGGGGGTTTATAACTTAACTGAAAAATTAATG
CTTCATCATAACATTTAAGCTATATCTAGAAAGTAGACTGGAGAACTGAGAAAATTACCCAG
GTAATTCAGGGAAAAAAAATATATATATATATAAATACCCCTACATTTGAAGTCAGAAA
ACTCTGAAAACTGAATTATCAAAGTCAATCATCTATAATGATCAAATTTACTGAACAATTG
TTAATTTATCCATTGTGCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTCA
ATAAAAATTGTTTTTTGAAATCCAGAAATGATTTAAAAAGAGGTCAGGTTTTTAACTATTTA
TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA
GATTCCTTTGAATATGTATTTACTTTAAAGACTGGAAAAAGCTCTTCCTGTCTTTTAGTAAAA
CATCCATATTTCATAACCTGATGTAAAATATGTTGTACTGTTTCCAATAGGTGAATATAAAC
TCAGTTTATCAATTAAAAA

70/75

FIGURE 69

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTTCACATGGGCACA
ATTTACACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTTG
TTCTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCA
AGCGCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCT
TTAATTAAGGGGTTACATCCAACCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCT
GCGTCACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGAC**ATG**TATAGACACAAAAA
CAGCTGGAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAAA
CATTGATTTTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCA
GCCCACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCAC
CGCTGCCCTGCCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGG
CAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGTAGTGACCTCCAG
GCCAGTGCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGC
ACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCT
TCTCCTCCTGCAAA**TAG**

71/75

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA44175
><subunit 1 of 1, 155 aa, 1 stop
><MW: 17194, pI: 10.44, NX(S/T): 0
MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLL
SGATATAALPLEGGPTGRDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVA
RRQEGAPPQQSARRDRMPCRNFFWKTFSSCK
```

Important features of the protein:

Transmembrane domain:

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

72/75

FIGURE 71

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCCTCC**ATG**GCGTGGAGCCTTGGGA
GCTGGCTGGGTGGCTGCCTGCTGGTGTGTCAGCATTGGGAATGGTACCACCTCCCGAAAATGTC
AGAATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGG
GAACCTGACTTTCACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATA
CTACCTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTC
AGGGCTGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCCTGTGGATGA
CACCATTATTGGACCCCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTT
TCTTAGCCCCATAAAATTGAGAATGAATACGAACTTGGACTATGAAGAATGTGTATAACTCA
TGGACTTATAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCA
GTATGACTTTGAGGTCCTCAGAAACCTGGAGCCATGGACAACCTATTGTGTTCAAGTTCGAG
GGTTTCTTCCTGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACC
CATGACGAAACGGTCCCCCTCCTGGATGGTGGCCGTCATCCTCATGGCCTCGGTCTTCATGGT
CTGCCTGGCACTCCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAAGACAAAGTACG
CCTTCTCCCCTAGGAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCAT
AACACACTTCTGTTTTTCTCCTTTCCATTGTCGGATGAGAATGATGTTTTTGACAAGCTAAG
TGTCATTGCAGAAGACTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGA
CCCCGCCTGGGCAGGGGCCCCAAAGC**TAG**GCTCTGAGAAGGAAACACACTCGGCTGGGCACA
GTGACGTACTCCATCTCACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGA
CCATCTGAGCCAGCCCCACATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACAT
TTTAAAGGCTGTCTTGCCAAAAATACTCCATTTGGGAACTCACTGCCTTATAAAGGCTTTCA
TGATGTTTTTCAGAAGTTGGCCACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAA
GATCATGTTTTAATTGTGAGAAACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCA
CCTTAGAGGTCGAGGCAGGCGGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAATA
TGGTGAAACCCAGTCTCTACTAAAAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTAT
AATCCCAGCTACTCGAGTGCCTGAGGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGA
GGTTGCAGTGAGCCGAGATAGCGGCACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCAT
CTCAAAAAAAAAAAAAAAAAAATTGTGAGAAACAGAAATACTTAAATGAGGAATAAGAATGG
AGATGTTACATCTGGTAGATGTAAACATTCTACCAGATTATGGATGGACTGATCTGAAATCG
ACCTCAACTCAAGGGTGGTCAGCTCAATGCTACACAGAGCACGGACTTTTGATTCTTTGCA
GTACTTTGAATTTATTTTTCTACCTATATATGTTTTATATGCTGCTGGTGCTCCATTAAAGT
TTTACTCTGTGTTGC

73/75

FIGURE 72

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF
QDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADDEHSDWVNITFCPVDDTIIGPPGMQVEVLA
DSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWT
YCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVPSPWMVAVILMASVFMVCLALLGCFSLWCV
YKKTKYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNP
DSCSLGTPPGQPQS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

CGAGCGCCAACCCGCTAGCGCCTGAATCCGGCGCTGCTGCCCGCTCGCCGCCCGCCG**ATG**GCCG
CGCGAGCCCCGCTGCTCGCCGCGTTGACCGCGCTCCTCGCCGCCCGCTGCTGGCGGAGAT
GCCCCGCCGGGCAAAATCGCGGTGGTTGGGGCTGGGATTGGGGGCTCTGCTGTGGCCCATTT
TCTCCAGCAGCACTTTGGACCTCGGGTGCAGATCGACGTGTACGAGAAGGGAACCGTGGGTG
GCCGCTTGGCCACCATCTCAGTCAACAAGCAGCACTATGAGAGCGGGGCTGCCTCCTTCCAC
TCCCTGAGCCTGCACATGCAGGACTTCGTCAAGCTGCTGGGGCTGAGGCACCGGCGCGAGGT
GGTGGGCAGGAGCGCCATCTTCGGCGGGGAGCACTTCATGCTGGAGGAGACTGACTGGTACC
TGCTGAACCTCTTCCGCCTCTGGTGGCACTATGGCATCAGCTTCCTGAGGCTGCAGATGTGG
GTGGAGGAGGTCATGGAGAAGTTCATGAGGATCTATAAGTACCAGGCCACGGCTATGCCTT
CTCGGGTGTGGAGGAGCTGCTCTACTACTGGGGGAGTCCACCTTTGTAAACATGACCCAGC
ACTCTGTGGCTGAGTCCCTGCTGCAGGTGGGCGTCACGCAGCGCTTTTATTGATGATGTCGTT
TCTGCTGTCTTGCGGGCCAGCTATGGCCAGTCAGCAGCGATGCCCGCCTTTGCAAGGAGCCAT
GTCAGTACCGGGGCCCAAGGCAGCCTGTGGTCTGTGGAAGGAGGCAATAAGCTGGTTTTGTT
CCGGTTTTGCTGAAGCTCACCAAGGCCAATGTGATCCATGCCACAGTGACCTCTGTGACCCTG
CACAGCACAGAGGGGAAAGCCCTGTACCAGGTGGCGTATGAGAATGAGGTAGGCAACAGCTC
TGACTTCTATGACATCGTGGTCATCGCCACCCCCCTGCACCTGGACAACAGCAGCAGCAACT
TAACCTTTGCAGGCTTCCACCCGCCCATTTGATGACGTGCAGGGCTCTTTCCAGCCCACCGTC
GTCTCCTTGGTCCACGGCTACCTCAACTCGTCTACTTCGGTTTCCAGACCCTAAGCTTTT
CCCCTTTGCCAACATCCTTACCACAGATTTCCCCAGCTTCTTCTGCACCTGGACAACATCT
GCCCTGTCAACATCTCTGCCAGCTTCCGGCGAAAGCAGCCCCAGGAGGCAGCTGTTTTGGCGA
GTCCAGTCCCCCAAGCCCCCTCTTTTCGGACCCAGCTAAAGACCCTGTTCCGTTCTTATTACTC
AGTGCAGACAGCTGAGTGGCAGGCCCATCCCCTCTATGGCTCCCGCCCCACGCTCCCGAGGT
TTGCACTCCATGACCAGCTCTTCTACCTCAATGCCCTGGAGTGGGCGGCCAGCTCCGTGGAG
GTGATGGCCGTGGCTGCCAAGAATGTGGCCTTGCTGGCTTACAACCGCTGGTACCAGGACCT
AGACAAGATTGATCAAAAAGATTTGATGCACAAGGTCAAGACTGAAGTGTGAGGGCTCTAGG
GAGAGCCTGGGAACCTTTCATCCCCCACTGAAGATGGATCATCCACACAGCAGCCCAGGACTGA
ATAAGCCATGCTCGCCCACCAGGCTTCTTTCTGACCCCTCATGTATCAAGCATCTCCAGGTG
ACCTACTGTCTGCCTATATTAAGGGTCCACACGGCGGCTGCTGCTTTTTTTTTTAAGGGGGAAA
GTAAGAAAAGAGAAGGAAATCCAAGCCAGTATATTTGTTTTATTTATTTTTTTTTTAAGAAGAA
AAAAGTTCATCTTCAAGGTGCTTCAGACTTGGTTTTCTTAGCTAGAAACCAGAAGACTACG
GGAGGGAATATAAGGCAGAGAACTATGAGTCTTATTTTATTACTGTTTTTCACTACCTACTC
CCACAATGGACAATCAATTGAGGCAACCTACAAGAAAACATTTACAACCAGATGGTTACAAA
TAAAGTAGAAGGGAAGATCAGAAAACCTAAGAAATGATCATAGCTCCTGGTTACTGTGGACT
TGATGGATTTGAAGTACCTAGTTTCAAGAACTCCCTAGTCACCATCTCCAAGCCTGTCAACATC
ACTGCATATTTGGAGGAGATGACTGTGGTAGGACCCAAGGAAGAGATGTGTGCCTGAATAGTC
GTCACCATATCTCCAAGCTTCCCTGGCAACCAGTGGGAAAAGAAACATGCGAGGCTGTAGGAA
GAGGGAAGCTCTTCCCTTGGCACCTAGAGGAATTAGCCATTCTCTTCTTATGCAAAGATTGA
GGAATGCAACAATATAAAGAAGAGAAGTCCCCAGATGTTAGAGAGCAGTCATATCTTACCCC
TAGATGTTTCTCCTCAGCAGAGAAGAAAGAAAGGTGTTGGGGTAGGATTCTTCAGAGGTTAGC
CTGGTACTTTCTCATCAGACACTAGCTTGAAGTAAGAGGAGAATTATGCTTTTCTTTGCTTT
TTCTACAAACCCTTAAAAATCACTTGTTTTAAAAAGAAAGTAAAAGCCCTTTTCATTCAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

75/75

FIGURE 74

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA116510

><subunit 1 of 1, 494 aa, 1 stop

><MW: 54646, pI: 7.27, NX(S/T): 6

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WYLLNLFRLWWHYGISFLRLQMWVEEVMEKFMRIYKYQAHGYAFSGVEELLYSLGESTFVNM
TQHSVAESLLQVGVTQRFIDDVVSAVLRASYGQSAAMPAFAGAMSLAGAQQGSLWSVEGGNKL
VCSGLLKLTKANVIHATVTSVTLHSTEGKALYQVAYENEVGNSSDFYDIVVIATPLHLDNSS
SNLTFAGFHPPIDDVQGSFQPTVVSLVHGYLNSSYFGFPDPKLFPPFANILTDFPSFFCTLD
NICPVNISASFRRKQPQEA AVWRVQSPKPLFRTQLKTLFRSYYSVQTAEWQAHPLYGSRPTL
PRFALHDQLFYLNLEWAASSVEVMAVA AKNVALLAYNRWYQDLDKIDQKDLMHKVKTEL

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 185-189, 290-294, 308-312, 312-316, 342-346, 378-382

N-myristoylation sites.

amino acids 33-39, 35-41, 38-44, 61-67, 64-70, 218-224, 234-240,
237-243, 429-435